Amendments

In the Claims:

Claim 1 (Currently amended): A method of screening for compounds which affect mRNA stability, comprising the steps of:

(a) providing a DNA expression system which, in the absence of the test compound, is capable of expressing a protein ~~having~~ which gives a detectable signal, wherein mRNA which codes for the protein and which is transcribed from the expression system comprises at least one copy of a mRNA instability sequence;

(b) contacting the DNA expression system with at least one test compound;

(c) measuring the detectable signal in the presence of the test compound; and

(d) comparing the measured detectable signal with a control;

wherein a decrease in the measured detectable signal compared to the control indicates a compound that decreases mRNA stability and an increase in the measured detectable signal compared to the control indicates a compound that increases mRNA stability, and wherein said DNA expression system comprises: 1) an expression cassette consisting of one or more reporter genes encoding said protein, a ~~and~~ 5′ UTR sequence, and a 3′ UTR ~~sequences~~ sequence of the reporter gene, wherein said 5′ UTR sequence and said 3′ UTR sequence comprise ~~comprising~~ operably-linked expression control elements; and 2) an instability region consisting of at least 20-100 nucleotides of the 3′ UTR of a gene sequence which confers instability to a mRNA, wherein said instability region is inserted into the 3′ UTR sequence of the reporter gene ~~said expression cassette~~, and wherein said instability region is

heterologous to the 3′ UTR sequence of the reporter gene.

Claim 2 (Canceled).

Claim 3 (Currently amended): A method for comparing the extent of mRNA degradation induced by two or more compounds, comprising the steps of:

(a) providing a DNA expression system, which in the absence of a test compound is capable of expressing a protein ~~having~~ which gives a detectable signal, wherein mRNA which codes for the protein and which is transcribed from the expression system, comprises at least one copy of a mRNA instability sequence;

(b) separately contacting the DNA expression system with two or more test compounds;

(c) measuring the detectable signal in the presence of each test compound; and

(d) comparing the measured detectable signals;

wherein the compound whose presence results in a lower measured detectable signal has induced a greater extent of mRNA degradation, and wherein said DNA expression system comprises: 1) an expression cassette consisting of one or more reporter genes encoding said protein, a ~~and~~ 5′ UTR sequence, and a 3′ UTR ~~sequences~~ sequence of the reporter gene, wherein said 5′ UTR sequence, and said 3′ UTR comprise ~~comprising~~ operably-linked expression control elements; and 2) an instability region consisting of at least 20-100 nucleotides of the 3′ UTR of a gene sequence which confers instability to a mRNA, wherein said instability region is inserted into the 3′ UTR sequence of the reporter gene ~~said~~

~~expression cassette~~, and wherein said instability is heterologous to the 3′ UTR sequence of the reporter gene.

Claim 4 (Currently amended): A reporter gene DNA expression system comprising: 1) an expression cassette consisting of one or more reporter genes encoding a protein ~~having~~ which gives a detectable signal, a ~~and~~ 5′ UTR sequence and a 3′ UTR ~~sequences~~ sequence of the reporter gene, wherein said 5′ UTR sequence and said 3′ UTR sequence comprise ~~comprising~~ operably-linked expression control elements; and 2) an instability region consisting of at least 20-100 nucleotides of the 3′ UTR of a gene sequence which confers instability to a mRNA, wherein said instability region is inserted into the 3′ UTR sequence of the reporter gene ~~said expression cassette~~, and wherein said instability region is heterologous to the 3′ UTR sequence of the reporter gene.

Claim 5 (Previously presented): A stably transfected cell line comprising the reporter gene DNA expression system of claim 4.

Claim 6 (Currently amended): An assay system for screening for compounds which ~~destabilise~~ destabilize mRNA comprising:

(a) the reporter gene DNA expression system of claim 4; and

(b) a control DNA expression system comprising said reporter gene coding for ~~expression of~~ a protein ~~having~~ which gives a detectable signal~~, wherein the gene comprises DNA coding for the amino acid sequence of the protein~~ together with a 5′

UTR sequence, and a 3′ UTR ~~sequences~~ sequence of the reporter gene, wherein said 5′ UTR sequence and said 3′ UTR sequence comprise ~~comprising~~ operably-linked expression control elements, but ~~lacking~~ lack any functional mRNA instability sequences.

Claim 7 (Previously presented): The assay system according to claim 6, wherein said reporter gene expression system and said control DNA expression system are provided in a stably transfected cell line.

Claim 8 (Currently amended): A stably transfected cell line comprising:

(a) the reporter gene DNA expression system of claim 4; and

(b) a control DNA expression system comprising a reporter gene coding for ~~expression of~~ a second protein ~~having~~ which gives a detectable signal~~, wherein the gene comprises DNA coding for the amino acid sequence of the protein~~ together with a 5′ UTR sequence, and a 3′ UTR ~~sequences~~ sequence of the reporter gene, wherein said 5′ UTR sequence and said 3′ UTR sequence comprise ~~comprising~~ operably-linked expression control elements, but ~~lacking~~ lack any functional mRNA instability sequences.

Claim 9 (Previously presented): An assay system for screening for compounds that destabilize mRNA comprising the stably transfected cell line according to claim 8.

Claims 10-14 (Canceled).

Claim 15 (Previously presented): The method according to claim 1, wherein said compounds are being screened for inducing mRNA degradation, and wherein a decrease in the measured detectable signal compared to said control indicates a compound that induces mRNA degradation.

Claim 16 (Previously presented): A reporter gene DNA expression system as in claim 4, wherein said instability region is from genes coding for cytokines, chemokines, nuclear transcription factors, protooncogenes, immediate early genes, cell cycle controlling genes, oxygenases, or genes involved in and controlling of apoptosis.

Claim 17 (Currently amended). A reporter gene DNA expression system as in claim 4, wherein said instability region is from genes coding for GM-CSF, ~~*c-fox,*~~ *c-fos*, *c-myc*, *c-jun*, *krox*-20, *nur*-77, *zif*268, bcl-2, β-IFN, uPA, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-13, TNF-α, MCP-1, syn1, β2-AR, E-selectin, VCAM-1, ICAM-1, Gro-α, Gro-β, MMP-1, MMP-2, collagenases, P-glycoproteins (MDR), MRPs, Pγh1 (PF mdr), COXII, or MIP-2α.

Claim 18 (New): A method of screening for compounds which affect mRNA stability, comprising the steps of:

(a) providing a DNA expression system which, in the absence of the test

compound, is capable of expressing a protein which gives a detectable signal, wherein mRNA which codes for the protein and which is transcribed from the expression system comprises at least one copy of a mRNA instability sequence;

(b) contacting the DNA expression system with at least one test compound;

(c) measuring the detectable signal in the presence of the test compound; and

(d) comparing the measured detectable signal with a control;

wherein a decrease in the measured detectable signal compared to the control indicates a compound that decreases mRNA stability and an increase in the measured detectable signal compared to the control indicates a compound that increases mRNA stability, and wherein said DNA expression system comprises: 1) an expression cassette consisting of one or more reporter genes encoding said protein, a 5′ UTR sequence, and a 3′ UTR sequence of the reporter gene, wherein said 5′ UTR sequence and said 3′ UTR sequence comprise operably-linked expression control elements; and 2) an instability region consisting of at least 20-100 nucleotides of the 3′ UTR of a gene sequence which confers instability to a mRNA, wherein said instability region is inserted into the 3′ UTR sequence of the reporter gene, wherein said instability region is heterologous to the 3′ UTR sequence of the reporter gene, and wherein said protein which gives a detectable signal is selected from the group consisting of a fluorescent protein and an enzyme.

Claim 19 (New): The method according to claim 18, wherein said protein which gives a detectable signal is a fluorescent protein.

Claim 20 (New): The method according to claim 19, wherein said fluorescent protein is green fluorescent protein.

Claim 21 (New): The method according to claim 18, wherein said protein which gives a detectable signal is an enzyme.

Claim 22 (New): The method according to claim 21, wherein said enzyme is selected from the group consisting of horseradish peroxidase, chloramphenicol acetyltransferase, alkaline phosphatase, secreted alkaline phosphatase, β-galactosidase and luciferase.

Claim 23 (New): A method for comparing the extent of mRNA degradation induced by two or more compounds, comprising the steps of:

(a) providing a DNA expression system, which in the absence of a test compound is capable of expressing a protein which gives a detectable signal, wherein mRNA which codes for the protein and which is transcribed from the expression system, comprises at least one copy of a mRNA instability sequence;

(b) separately contacting the DNA expression system with two or more test compounds;

(c) measuring the detectable signal in the presence of each test compound; and

(d) comparing the measured detectable signals;

wherein the compound whose presence results in a lower measured detectable signal has induced a greater extent of mRNA degradation, and wherein said DNA expression system comprises: 1) an expression cassette consisting of one or more reporter genes encoding said protein, a 5′ UTR sequence, and a 3′ UTR sequences of the reporter gene, wherein said 5′

UTR sequence and said 3′ UTR sequence comprise operably-linked expression control elements; and 2) an instability region consisting of at least 20-100 nucleotides of the 3'UTR of a gene sequence which confers instability to a mRNA, wherein said instability region is inserted into the 3′ UTR sequence of the reporter gene, wherein said instability region is heterologous to the 3′ UTR sequence of the reporter gene, and wherein said protein which gives a detectable signal is selected from the group consisting of a fluorescent protein and an enzyme.

Claim 24 (New): The method according to claim 23, wherein said protein which gives a detectable signal is a fluorescent protein.

Claim 25 (New): The method according to claim 24, wherein said fluorescent protein is green fluorescent protein.

Claim 26 (New): The method according to claim 23, wherein said protein which gives a detectable signal is an enzyme.

Claim 27 (New): The method according to claim 26, wherein said enzyme is selected from the group consisting of horseradish peroxidase, chloramphenicol acetyltransferase, alkaline phosphatase, secreted alkaline phosphatase, β-galactosidase and luciferase.

Claim 28 (New): A reporter gene DNA expression system comprising: 1) an

expression cassette consisting of one or more reporter genes encoding a protein which gives a detectable signal, a 5′ UTR sequence, and a 3′ UTR sequence of the reporter gene, wherein said 5′ UTR sequence and said 3′ UTR sequence comprise operably-linked expression control elements; and 2) an instability region consisting of at least 20-100 nucleotides of the 3′ UTR of a gene sequence which confers instability to a mRNA, wherein said instability region is inserted into the 3′ UTR sequence of the reporter gene, said instability region being heterologous to the 3′ UTR sequence of the reporter gene, and wherein said protein which gives a detectable signal is selected from the group consisting of a fluorescent protein and an enzyme.

Claim 29 (New): The reporter gene DNA expression system according to claim 28, wherein said protein which gives a detectable signal is a fluorescent protein.

Claim 30 (New): The reporter gene DNA expression system according to claim 29, wherein said fluorescent protein is green fluorescent protein.

Claim 31 (New): The reporter gene DNA expression system according to claim 28, wherein said protein which gives a detectable signal is an enzyme.

Claim 32 (New): The reporter gene DNA expression system according to claim 31, wherein said enzyme is selected from the group consisting of horseradish peroxidase, chloramphenicol acetyltransferase, alkaline phosphatase, secreted alkaline phosphatase, β-

galactosidase and luciferase.

Claim 33 (New): A stably transfected cell line comprising the reporter gene DNA expression system of claim 28.

Claim 34 (New): An assay system for screening for compounds which destabilize mRNA comprising:

(a) the reporter gene DNA expression system of claim 28; and

(b) a control DNA expression system comprising said reporter gene coding for a protein which gives a detectable signal, together with a 5′ UTR sequence, and a 3′ UTR sequence of the reporter gene, wherein said 5′ UTR sequence and said 3′ UTR sequence comprise operably-linked expression control elements, but lack any functional mRNA instability sequences, wherein said protein which gives a detectable signal is selected from the group consisting of a fluorescent protein and an enzyme.

Claim 35 (New): The assay system according to claim 34, wherein said protein which gives a detectable signal is a fluorescent protein.

Claim 36 (New): The assay system according to claim 35, wherein said fluorescent protein is green fluorescent protein.

Claim 37 (New): The assay system according to claim 34, wherein said protein which gives a detectable signal is an enzyme.

Claim 38 (New): The assay system according to claim 37, wherein said enzyme is selected from the group consisting of horseradish peroxidase, chloramphenicol acetyltransferase, alkaline phosphatase, secreted alkaline phosphatase, β-galactosidase and luciferase.

Claim 39 (New): The assay system according to claim 34, wherein said reporter gene expression system and said control DNA expression system are provided in a stably transfected cell line.

Claim 40 (New): A stably transfected cell line comprising:

(a) the reporter gene DNA expression system of claim 28; and

(b) a control DNA expression system comprising a reporter gene coding for a second protein which gives a detectable signal together with a 5′ UTR sequence, and a 3′ UTR sequence of the reporter gene, wherein said 5′ UTR sequence and said 3′ UTR sequence comprise operably-linked expression control elements, but lack any functional mRNA instability sequences, wherein said protein which gives a detectable signal is selected from the group consisting of a fluorescent protein and an enzyme.

Claim 41 (New): The stably transfected cell line according to claim 40, wherein said

protein which gives a detectable signal is a fluorescent protein.

Claim 42 (New): The stably transfected cell line according to claim 41, wherein said fluorescent protein is green fluorescent protein.

Claim 43 (New): The stably transfected cell line according to claim 40, wherein said protein which gives a detectable signal is an enzyme.

Claim 44 (New): The stably transfected cell line according to claim 43, wherein said enzyme is selected from the group consisting of horseradish peroxidase, chloramphenicol acetyltransferase, alkaline phosphatase, secreted alkaline phosphatase, β-galactosidase and luciferase.

Claim 45 (New): An assay system for screening for compounds that destabilize mRNA comprising the stably transfected cell line according to claim 40.

Claim 46 (New): The method according to claim 18, wherein said compounds are being screened for inducing mRNA degradation, and wherein a decrease in the measured detectable signal compared to said control indicates a compound that induces mRNA degradation.

Claim 47 (New): A reporter gene DNA expression system as in claim 28, wherein said instability region is derived from genes coding for cytokines, chemokines, nuclear transcription factors, protooncogenes, immediate early genes, cell cycle controlling genes, oxygenases, or genes involved in and controlling of apoptosis.

Claim 48 (New): A reporter gene DNA expression system as in claim 28, wherein said instability region is derived from genes coding for GM-CSF, *c-fos*, *c-myc*, *c-jun*, *krox*-20, *nur*-77, *zif*268, bcl-2, β-IFN, uPA, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-13, TNF-α, MCP-1, syn1, β2-AR, E-selectin, VCAM-1, ICAM-1, Gro-α, GRo-β, MMP-1, MMP-2, collagenases, P-glycoproteins (MDR), MRPs, Pγh1 (PF mdr), COXII, or MIP-2α.